

--	--	--	--	--	--	--	--	--	--

MULTIMEDIA UNIVERSITY

FINAL EXAMINATION

TRIMESTER 2, 2015/2016

HPB2011 – BIOINFORMATICS PROGRAMMING I
(All sections / Groups)

07 March 2016
09:00-11:00 AM
(2 hours)

INSTRUCTIONS TO STUDENTS

1. This question paper consists of 6 pages including cover page and 5 questions only.
2. Attempt **FOUR** out of **FIVE** questions. All questions carry equal marks (10), and the distribution of the marks for each question is given.
3. Please write all your answers in the Answer Booklet provided.

QUESTION 1 [10 marks]

- a) Briefly discuss pairwise sequence alignment. Why is it used? What does it show? What are the 3 main types of methods used for it? [4 marks]

- b) Given the following 2 nucleotide sequences, find their best alignment using dynamic programming and traceback, using Needleman-Wunsch algorithm (global) [4 marks]

Seq1: CGCGAATCAGT

Seq2: TGCTAAGAC

Match = 2, mismatch = 0, gap = -2

- c) Determine the alignment score for each of the following sequence pairs.

Global alignment: match score = +1, mismatch score = 0, gap penalty = -2.

- i. ~TCTGTACGCGATCATGT
TAGC~GTCCGATAT~A~~

Global alignment: match score = +1, mismatch score = -1, gap origination penalty = -3, gap length penalty = -1

- ii. AGATAGAAACTGATATATA
AGA~A~A~ACAGAG~T~~

[2 marks]

Continue....

QUESTION 2 [10 marks]

a) What is Chou-Fasman. What are differences between the Chou-Fasman and the GOR methods for estimating secondary structures? [4 marks]

b) Given the following part of the Chou-Fasman table,

Name		P(a)	P(b)	P(turn)
Ala	A	142	83	66
Cys	C	70	119	119
Asp	D	101	54	146
Glu	E	151	37	74
Phe	F	113	138	60
Gly	G	57	75	156
His	H	100	87	95
Iso	I	108	160	47
Lys	K	114	74	101
Leu	L	121	130	59
Met	M	145	105	60
Asn	N	67	89	156
Pro	P	57	55	152
Gln	Q	111	110	98
Arg	R	98	93	95
Ser	S	77	75	143
Thr	T	83	119	96
Val	V	106	170	50
Try	W	108	137	96
Tyr	Y	69	147	114

calculate the secondary structure of the following sequence, only for α -helices and β -sheets (not for turns): **R G P T C W P A E N K L** . Give your answer as a table.

[6 marks]

Continue....

QUESTION 3 [10 marks]

- a) Write the attributes of a “public class FASTAobject” which is the content of a file in FASTA format. For each attribute, explain in a comment (//) what it is. Write at least 2 “get” methods which return particular pieces of information from a FASTAobject object.

[4 marks]

- b) Write correct Java code to

1. get the path and name of a FASTA file from the user (command line)
2. Open the file using “try ... catch”
3. Create a “FASTAobject” object as in Question 2a
4. Read information from the FASTA file, one line at a time, and store it in the correct attribute in the FASTAobject. To parse the first line into accession number and “description” you might need String methods “indexOf(…)” and “substring(…)”
5. Close the FASTA file when you are finished

[6 marks]

Continue....

QUESTION 4 [10 marks]

a) Determine the output of the following code:

[4 marks]

```
public class Animal {
    public static int times = 0;
    public Animal() {
        System.out.println("A new animal has been
created!");
        times++;
    }
    public void sleep() {
        System.out.println("An animal sleeps...");
    }
    ///////////////////////////////////////////////////
    public class Bird extends Animal {
        public Bird() {
            super();
            System.out.println("A new bird has been
created");
            System.out.println (times);
        }
        public void sleep() {
            System.out.println("A bird sleeps...");
        }
    }
    ///////////////////////////////////////////////////
    public class Dog extends Animal {
        public Dog() {
            super();
            System.out.println("A new dog has been created!");
            System.out.println (times);
        }
        public void sleep() {
            System.out.println("A dog sleeps...");
        }
    }
    ///////////////////////////////////////////////////
    public class MainClass {
        public static void main(String[] args) {
            Animal animal = new Animal();
            Bird bird = new Bird();
            Animal d = new Dog();

            animal.sleep();
            bird.sleep();
            d.sleep();}}
}
```

b) Write a function "echoR1_Exist(seq)" which gets a sequence as the function parameter and checks whether restriction site EcoRI = "GAATTC" is present in the sequence. This function returns a boolean value to show if the sequence contains the restriction site. Make sure all the types (return and parameter types) are correctly mentioned.

[4 marks]

c) List down 4 major components of Object-Oriented programming

[2 marks]

Continue....

QUESTION 5 [10 marks]

- a) Define a function *complement(seq)* that finds the complement of input sequence *seq*. The function gets a sequence through a parameter and returns the complement of the sequence. [3 marks]

Hint:

- *complement_map = {'c': 'g', 'g': 'c', 'a': 't', 't': 'a'}*
- *example seq=aaaccc; output=tttggg*

- b) Write a java interface “Shape” which contains a String attribute label (you have to initiate the attribute). The interface has two functions draw() which returns nothing, and getArea() which returns the area of the Shape. Write a class called Circle and uses the interface Shape. The Circle class has an attribute “radius”. THINK ABOUT any functions you need to write for the class Circle. [3 marks]

- c) Explain briefly the following terms in Java GUI layouts. Draw the layout for your explanation and write the Java code for initiating these layouts.
BorderLayout, FlowLayout, GridLayout [4 marks]

End of paper